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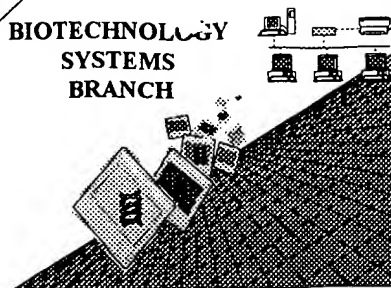
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0400  
4/5/01

**RAW SEQUENCE LISTING**  
**ERROR REPORT**

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



0400  
02-67-01  
3/24/01

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/757,100

Source: O/PE

Date Processed by STIC: 2/13/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**

**<http://www.uspto.gov/web/offices/pac/checker>**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/757,100

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2      Wrapped Aminos      The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3      Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4      Misaligned Amino Acid Numbering      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5      Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6      Variable Length      Sequence(s)      contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7      PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)     . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8      Skipped Sequences (OLD RULES)      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9      Skipped Sequences (NEW RULES)      Sequence(s)      missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 10      Use of n's or Xaa's (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11      Use of <213>Organism (NEW RULES)      Sequence(s)      are missing this mandatory field or its response.
- 12      Use of <220>Feature (NEW RULES)      Sequence(s)      are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13      PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING                      DATE: 02/13/2001  
 PATENT APPLICATION: US/09/757,100                      TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw  
 Output Set: N:\CRF3\02132001\I757100.raw

**Does Not Comply  
 Corrected Diskette Needed**

1 <110> APPLICANT: Monia, Brett P.  
 2     Gaarde, William A.  
 3     Nero, Pamela S.  
 4 <120> TITLE OF INVENTION: Antisense Modulation of Focal Adhesion Kinase  
 5     Expression  
 6 <130> FILE REFERENCE: ISPH-0533  
 7 <140> CURRENT APPLICATION NUMBER: US/09/757,100  
 8 <141> CURRENT FILING DATE: 2001-01-09  
 9 <150> PRIOR APPLICATION NUMBER: 09/377,310  
 10 <151> PRIOR FILING DATE: 1999-08-19  
 11 <150> PRIOR APPLICATION NUMBER: PCT/US00/18999  
 12 <151> PRIOR FILING DATE: 2000-07-13  
 13 <160> NUMBER OF SEQ ID NOS: 44  
 14 <170> SOFTWARE: PatentIn Ver. 2.0

#### ERRORED SEQUENCES

16 <210> SEQ ID NO: 1  
 17 <211> LENGTH: 3791  
 18 <212> TYPE: DNA  
 19 <213> ORGANISM: Homo sapiens  
 20 <220> FEATURE:  
 21 <221> NAME/KEY: CDS  
 22 <222> LOCATION: (233)..(3391)  
 23 <300> PUBLICATION INFORMATION:  
 24 <303> JOURNAL: DNA  
 25 <304> VOLUME: 12  
 26 <305> ISSUE: 9  
 27 <306> PAGES: 823-830  
 28 <307> DATE: 1993-11  
 29 <308> DATABASE ACCESSION NO: L13616/Genbank  
 30 <309> DATABASE ENTRY DATE: 1995-01-02  
 31 <400> SEQUENCE: 1

E--> 32     cgaccactgt   gagcccgcg   cgtgaggcgt   cgggaggaag   cgcggctgct  
 33     gtcgcccagc 60  
 E--> 34     gccgccccgt   cgctgtctgc   ctctgcttca   cggcgccgag   ccgcgggtccg  
 35     agcagaactg 120  
 E--> 36     gggctccctt   gcatcttcca   gttacaaatt   cagtgccttc   tgcagtttcc  
 37     ccagagctcc 180  
 E--> 38     tcaagaataa   cggaagggag   aatatgacag   atacctagca   tctagcaaaa   ta  
 39     atg gca 238  
 40     Met Ala  
 41     1  
 E--> 42     gct gct tac ctt gac ccc aac ttg aat cac aca cca aat tcg agt  
 43     act     286  
 44     Ala Ala Tyr Leu Asp Pro Asn Leu Asn His Thr Pro Asn Ser Ser

*global error*

*(see item 1 on Error  
 Summary Sheet)*

*format error*

*→ 60*

*→ 120*

## RAW SEQUENCE LISTING

DATE: 02/13/2001

PATENT APPLICATION: US/09/757,100

TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw

Output Set: N:\CRF3\02132001\I757100.raw

```

W--> 45      Thr
W--> 46              5              10              15
E--> 47      aag act cac ctg ggt act ggt atg gaa cgt tct cct ggt gca atg
48      gag      334
49      Lys Thr His Leu Gly Thr Gly Met Glu Arg Ser Pro Gly Ala Met
W--> 50      Glu
W--> 51              20              25              30
E--> 52      cga gta tta aag gtc ttt cat tat ttt gaa agc aat agt gag cca
53      acc      382
54      Arg Val Leu Lys Val Phe His Tyr Phe Glu Ser Asn Ser Glu Pro
W--> 55      Thr
W--> 56              35              40              45
E--> 57      50
E--> 58      acc tgg gcc agt att atc agg cat gga gat gct act gat gtc agg
59      ggc      430
60      Thr Trp Ala Ser Ile Ile Arg His Gly Asp Ala Thr Asp Val Arg
W--> 61      Gly
W--> 62              55              60              65
E--> 63      atc att cag aag ata gtg gac agt cac aaa gta aag cat gtg gcc
64      tgc      478
65      Ile Ile Gln Lys Ile Val Asp Ser His Lys Val Lys His Val Ala
W--> 66      Cys
W--> 67              70              75              80
E--> 68      tat gga ttc cgc ctc agt cac ctg cgg tca gag gag gtt cac tgg
69      ctt      526
70      Tyr Gly Phe Arg Leu Ser His Leu Arg Ser Glu Glu Val His Trp
W--> 71      Leu
W--> 72              85              90              95
E--> 73      cac gtg gat atg ggc gtc tcc agt gtg agg gag aag tat gag ctt
74      gct      574
75      His Val Asp Met Gly Val Ser Ser Val Arg Glu Lys Tyr Glu Leu
W--> 76      Ala
W--> 77              100              105              110
E--> 78      cac cca cca gag gag tgg aaa tat gaa ttg aga att cgt tat ttg
79      cca      622
80      His Pro Pro Glu Glu Trp Lys Tyr Glu Leu Arg Ile Arg Tyr Leu
W--> 81      Pro
W--> 82              115              120              125
E--> 83      130
E--> 84      aaa gga ttt cta aac cag ttt act gaa gat aag cca act ttg aat
85      ttc      670
86      Lys Gly Phe Leu Asn Gln Phe Thr Glu Asp Lys Pro Thr Leu Asn
W--> 87      Phe
W--> 88              135              140              145
E--> 89      ttc tat caa cag gtg aag agc gat tat atg tta gag ata gct gat
90      caa      718
91      Phe Tyr Gln Gln Val Lys Ser Asp Tyr Met Leu Glu Ile Ala Asp
W--> 92      Gln
W--> 93              150              155              160

```

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DATE: 02/13/2001

PATENT APPLICATION: US/09/757,100

TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw

Output Set: N:\CRF3\02132001\I757100.raw

```

E--> 94      gtg gac cag gaa att gct ttg aag ttg ggt tgt cta gaa ata cgg
          95      cga      766
          96      Val Asp Gln Glu Ile Ala Leu Lys Leu Gly Cys Leu Glu Ile Arg
W--> 97      Arg
          W--> 98      165                      170                      175
E--> 99      tca tac tgg gag atg cgg ggc aat gca cta gaa aag aag tct aac
          100      tat      814
          101      Ser Tyr Trp Glu Met Arg Gly Asn Ala Leu Glu Lys Lys Ser Asn
W--> 102      Tyr
          W--> 103      180                      185                      190
E--> 104      gaa gta tta gaa aaa gat gtt ggt tta aag cga ttt ttt cct aag
          105      agt      862
          106      Glu Val Leu Glu Lys Asp Val Gly Leu Lys Arg Phe Phe Pro Lys
W--> 107      Ser
          W--> 108      195                      200                      205
E--> 109      210
E--> 110      tta ctg gat tct gtc aag gcc aaa aca cta aga aaa ctg atc caa
          111      caa      910
          112      Leu Leu Asp Ser Val Lys Ala Lys Thr Leu Arg Lys Leu Ile Gln
W--> 113      Gln
          W--> 114      215                      220                      225
E--> 115      aca ttt aga caa ttt gcc aac ctt aat aga gaa gaa agt att ctg
          116      aaa      958
          117      Thr Phe Arg Gln Phe Ala Asn Leu Asn Arg Glu Glu Ser Ile Leu
W--> 118      Lys
          W--> 119      230                      235                      240
E--> 120      ttc ttt gag atc ctg tct cca gtc tac aga ttt gat aag gaa tgc
          121      ttc      1006
          122      Phe Phe Glu Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys Glu Cys
W--> 123      Phe
          W--> 124      245                      250                      255
E--> 125      aag tgt gct ctt ggt tca agc tgg att att tca gtg gaa ctg gca
          126      atc      1054
          127      Lys Cys Ala Leu Gly Ser Ser Trp Ile Ile Ser Val Glu Leu Ala
W--> 128      Ile
          W--> 129      260                      265                      270
E--> 130      ggc cca gaa gaa gga atc agt tac cta acg gac aag ggc tgc aat
          131      ccc      1102
          132      Gly Pro Glu Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly Cys Asn
W--> 133      Pro
          W--> 134      275                      280                      285
E--> 135      290
E--> 136      aca cat ctt gct gac ttc act caa gtg caa acc att cag tat tca
          137      aac      1150
          138      Thr His Leu Ala Asp Phe Thr Gln Val Gln Thr Ile Gln Tyr Ser
W--> 139      Asn
          W--> 140      295                      300                      305
E--> 141      agt gaa gac aag gac aga aaa gga atg cta caa cta aaa ata gca
          142      ggt      1198

```

*same*

RAW SEQUENCE LISTING                      DATE: 02/13/2001  
 PATENT APPLICATION: US/09/757,100              TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw  
 Output Set: N:\CRF3\02132001\I757100.raw

```

143      Ser Glu Asp Lys Asp Arg Lys Gly Met Leu Gln Leu Lys Ile Ala
W--> 144      Gly
145      310                      315                      320
E--> 146      gca ccc gag cct ctg aca gtg acg gca cca tcc cta acc att gcg
147      gag 1246
148      Ala Pro Glu Pro Leu Thr Val Thr Ala Pro Ser Leu Thr Ile Ala
W--> 149      Glu
150      325                      330                      335
E--> 151      aat atg gct gac cta ata gat ggg tac tgc cgg ctg gtg aat gga
152      acc 1294
153      Asn Met Ala Asp Leu Ile Asp Gly Tyr Cys Arg Leu Val Asn Gly
W--> 154      Thr
155      340                      345                      350
E--> 156      tcg cag tca ttt atc atc aga cct cag aaa gaa ggt gaa cgg gct
157      ttg 1342
158      Ser Gln Ser Phe Ile Ile Arg Pro Gln Lys Glu Gly Glu Arg Ala
W--> 159      Leu
160      355                      360                      365
E--> 161      370
E--> 162      cca tca ata cca aag ttg gcc aac agc gaa aag caa ggc atg cgg
163      aca 1390
164      Pro Ser Ile Pro Lys Leu Ala Asn Ser Glu Lys Gln Gly Met Arg
W--> 165      Thr
166      375                      380                      385
E--> 167      cac gcc gtc tct gtg tca gaa aca gat gat tat gct gag att ata
168      gat 1438
169      His Ala Val Ser Val Ser Glu Thr Asp Asp Tyr Ala Glu Ile Ile
W--> 170      Asp
171      390                      395                      400
E--> 172      gaa gaa gat act tac acc atg ccc tca acc agg gat tat gag att
173      caa 1486
174      Glu Glu Asp Thr Tyr Thr Met Pro Ser Thr Arg Asp Tyr Glu Ile
W--> 175      Gln
176      405                      410                      415
E--> 177      aga gaa aga ata gaa ctt gga cga tgt att gga gaa ggc caa ttt
178      gga 1534
179      Arg Glu Arg Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly Gln Phe
W--> 180      Gly
181      420                      425                      430
E--> 182      gat gta cat caa ggc att tat atg agt cca gag aat cca gct ttg
183      gcg 1582
184      Asp Val His Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro Ala Leu
W--> 185      Ala
186      435                      440                      445
E--> 187      450
E--> 188      gtt gca att aaa aca tgt aaa aac tgt act tcg gac agc gtg aga
189      gag 1630
190      Val Ala Ile Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser Val Arg
W--> 191      Glu

```

*same*

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Input Set : N:\Crf3\02052001\I757100.raw  
 Output Set: N:\CRF3\02132001\I757100.raw

```

W--> 192          455          460          465
E--> 193    aaa ttt ctt caa gaa gcc tta aca atg cgt cag ttt gac cat cct
      194    cat 1678
      195    Lys Phe Leu Gln Glu Ala Leu Thr Met Arg Gln Phe Asp His Pro
W--> 196    His
W--> 197          470          475          480
E--> 198    att gtg aag ctg att gga gtc atc aca gag aat cct gtc tgg ata
      199    atc 1726
      200    Ile Val Lys Leu Ile Gly Val Ile Thr Glu Asn Pro Val Trp Ile
W--> 201    Ile
W--> 202          485          490          495
E--> 203    atg gag ctg tgc aca ctt gga gag ctg agg tca ttt ttg caa gta
      204    agg 1774
      205    Met Glu Leu Cys Thr Leu Gly Glu Leu Arg Ser Phe Leu Gln Val
W--> 206    Arg
W--> 207          500          505          510
E--> 208    aaa tac agt ttg gat cta gca tct ttg atc ctg tat gcc tat cag
      209    ctt 1822
      210    Lys Tyr Ser Leu Asp Leu Ala Ser Leu Ile Leu Tyr Ala Tyr Gln
W--> 211    Leu
W--> 212          515          520          525
E--> 213    530
E--> 214    agt aca gct ctt gca tat cta gag agc aaa aga ttt gta cac agg
      215    gac 1870
      216    Ser Thr Ala Leu Ala Tyr Leu Glu Ser Lys Arg Phe Val His Arg
W--> 217    Asp
W--> 218          535          540          545
E--> 219    att gct gct cgg aat gtt ctg gtg tcc tca aat gat tgt gta aaa
      220    tta 1918
      221    Ile Ala Ala Arg Asn Val Leu Val Ser Ser Asn Asp Cys Val Lys
W--> 222    Leu
W--> 223          550          555          560
E--> 224    gga gac ttt gga tta tcc cga tat atg gaa gat agt act tac tac
      225    aaa 1966
      226    Gly Asp Phe Gly Leu Ser Arg Tyr Met Glu Asp Ser Thr Tyr Tyr
W--> 227    Lys
W--> 228          565          570          575
E--> 229    gct tcc aaa gga aaa ttg cct att aaa tgg atg gct cca gag tca
      230    atc 2014
      231    Ala Ser Lys Gly Lys Leu Pro Ile Lys Trp Met Ala Pro Glu Ser
W--> 232    Ile
W--> 233          580          585          590
E--> 234    aat ttt cga cgt ttt acc tca gct agt gac gta tgg atg ttt ggt
      235    gtg 2062
      236    Asn Phe Arg Arg Phe Thr Ser Ala Ser Asp Val Trp Met Phe Gly
W--> 237    Val
W--> 238          595          600          605
E--> 239    610
E--> 240    tgt atg tgg gag ata ctg atg cat ggt gtg aag cct ttt caa gga

```

*same*



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DATE: 02/13/2001

PATENT APPLICATION: US/09/757,100

TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw

Output Set: N:\CRF3\02132001\I757100.raw

```

241      gtg      2110
242      Cys Met Trp Glu Ile Leu Met His Gly Val Lys Pro Phe Gln Gly
W--> 243      Val
W--> 244                  615                      620                      625
E--> 245      aag aac aat gat gta atc ggt cga att gaa aat ggg gaa aga tta
246      cca      2158
247      Lys Asn Asn Asp Val Ile Gly Arg Ile Glu Asn Gly Glu Arg Leu
W--> 248      Pro
W--> 249                  630                      635                      640
E--> 250      atg cct cca aat tgt cct cct acc ctc tac agc ctt atg acg aaa
251      tgc      2206
252      Met Pro Pro Asn Cys Pro Pro Thr Leu Tyr Ser Leu Met Thr Lys
W--> 253      Cys
W--> 254                  645                      650                      655
E--> 255      tgg gcc tat gac ccc agc agg cgg ccc agg ttt act gaa ctt aaa
256      gct      2254
257      Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu Leu Lys
W--> 258      Ala
W--> 259                  660                      665                      670
E--> 260      cag ctc agc aca atc ctg gag gaa gag aag gct cag caa gaa gag
261      cgc      2302
262      Gln Leu Ser Thr Ile Leu Glu Glu Glu Lys Ala Gln Gln Glu Glu
W--> 263      Arg
W--> 264                  675                      680                      685
E--> 265      690
E--> 266      atg agg atg gag tcc aga aga cag gcc aca gtg tcc tgg gac tcc
267      gga      2350
268      Met Arg Met Glu Ser Arg Arg Gln Ala Thr Val Ser Trp Asp Ser
W--> 269      Gly
W--> 270                  695                      700                      705
E--> 271      ggg tct gat gaa gca ccg ccc aag ccc agc aga ccg ggt tat ccc
272      agt      2398
273      Gly Ser Asp Glu Ala Pro Pro Lys Pro Ser Arg Pro Gly Tyr Pro
W--> 274      Ser
W--> 275                  710                      715                      720
E--> 276      ccg agg tcc agc gaa gga ttt tat ccc agc cca cag cac atg gta
277      caa      2446
278      Pro Arg Ser Ser Glu Gly Phe Tyr Pro Ser Pro Gln His Met Val
W--> 279      Gln
W--> 280                  725                      730                      735
E--> 281      acc aat cat tac cag gtt tct ggc tac cct ggt tca cat gga atc
282      aca      2494
283      Thr Asn His Tyr Gln Val Ser Gly Tyr Pro Gly Ser His Gly Ile
W--> 284      Thr
W--> 285                  740                      745                      750
E--> 286      gcc atg gct ggc agc atc tat cca ggt cag gca tct ctt ttg gac
287      caa      2542
288      Ala Met Ala Gly Ser Ile Tyr Pro Gly Gln Ala Ser Leu Leu Asp
W--> 289      Gln

```

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Input Set : N:\Crf3\02052001\I757100.raw

Output Set: N:\CRF3\02132001\I757100.raw

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W--> 290      755                      760                      765
E--> 291      770
E--> 292      aca gat tca tgg aat cat aga cct cag gag ata gca atg tgg cag
293      ccc      2590
294      Thr Asp Ser Trp Asn His Arg Pro Gln Glu Ile Ala Met Trp Gln
W--> 295      Pro
W--> 296                      775                      780                      785
E--> 297      aat gtg gag gac tct aca gta ttg gac ctg cga ggg att ggg caa
298      gtg      2638
299      Asn Val Glu Asp Ser Thr Val Leu Asp Leu Arg Gly Ile Gly Gln
W--> 300      Val
W--> 301                      790                      795                      800
E--> 302      ttg cca acc cat ctg atg gaa gag cgt cta atc cga cag caa cag
303      gaa      2686
304      Leu Pro Thr His Leu Met Glu Glu Arg Leu Ile Arg Gln Gln Gln
W--> 305      Glu
W--> 306                      805                      810                      815
E--> 307      atg gaa gaa gat cag cgc tgg ctg gaa aaa gag gaa aga ttt ctg
308      aaa      2734
309      Met Glu Glu Asp Gln Arg Trp Leu Glu Lys Glu Glu Arg Phe Leu
W--> 310      Lys
W--> 311      820                      825                      830
E--> 312      cct gat gtg aga ctc tct cga ggc agt att gac agg gag gat gga
313      agt      2782
314      Pro Asp Val Arg Leu Ser Arg Gly Ser Ile Asp Arg Glu Asp Gly
W--> 315      Ser
W--> 316      835                      840                      845
E--> 317      850
E--> 318      ctt cag ggt ccg att gga aac caa cat ata tat cag cct gtg ggt
319      aaa      2830
320      Leu Gln Gly Pro Ile Gly Asn Gln His Ile Tyr Gln Pro Val Gly
W--> 321      Lys
W--> 322                      855                      860                      865
E--> 323      cca gat cct gca gct cca cca aag aaa ccg cct cgc cct gga gct
324      ccc      2878
325      Pro Asp Pro Ala Ala Pro Pro Lys Lys Pro Pro Arg Pro Gly Ala
W--> 326      Pro
W--> 327                      870                      875                      880
E--> 328      ggt cat ctg gga agc ctt gcc agc ctc agc agc cct gct gac agc
329      tac      2926
330      Gly His Leu Gly Ser Leu Ala Ser Leu Ser Ser Pro Ala Asp Ser
W--> 331      Tyr
W--> 332                      885                      890                      895
E--> 333      aac gag ggt gtc aag ctt cag ccc cag gaa atc agc ccc cct cct
334      act      2974
335      Asn Glu Gly Val Lys Leu Gln Pro Gln Glu Ile Ser Pro Pro Pro
W--> 336      Thr
W--> 337      900                      905                      910
E--> 338      gcc aac ctg gac cgg tcg aat gat aag gtg tac gag aat gtg acg

```

## RAW SEQUENCE LISTING

DATE: 02/13/2001

PATENT APPLICATION: US/09/757,100

TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw

Output Set: N:\CRF3\02132001\I757100.raw

```

339      ggc      3022
340      Ala Asn Leu Asp Arg Ser Asn Asp Lys Val Tyr Glu Asn Val Thr
W--> 341      Gly
W--> 342      915                      920                      925
E--> 343      930
E--> 344      ctg gtg aaa gct gtc atc gag atg tcc agt aaa atc cag cca gcc
345      cca      3070
346      Leu Val Lys Ala Val Ile Glu Met Ser Ser Lys Ile Gln Pro Ala
W--> 347      Pro
W--> 348                      935                      940                      945
E--> 349      cca gag gag tat gtc cct atg gtg aag gaa gtc ggc ttg gcc ctg
350      agg      3118
351      Pro Glu Glu Tyr Val Pro Met Val Lys Glu Val Gly Leu Ala Leu
W--> 352      Arg
W--> 353                      950                      955                      960
E--> 354      aca tta ttg gcc act gtg gat gag acc att ccc ctc cta cca gcc
355      agc      3166
356      Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro Leu Leu Pro Ala
W--> 357      Ser
W--> 358                      965                      970                      975
E--> 359      acc cac cga gag att gag atg gca cag aag cta ttg aac tct gac
360      ctg      3214
361      Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu Leu Asn Ser Asp
W--> 362      Leu
W--> 363      980                      985                      990
E--> 364      ggt gag ctc atc aac aag atg aaa ctg gcc cag cag tat gtc atg
365      acc      3262
366      Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln Gln Tyr Val Met
W--> 367      Thr
W--> 368                      995                      1000                      1005
E--> 369      1010
E--> 370      agc ctc cag caa gag tac aaa aag caa atg ctg act gct gct cac
371      gcc      3310
372      Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu Thr Ala Ala His
W--> 373      Ala
W--> 374                      1015                      1020                      1025
E--> 375      ctg gct gtg gat gcc aaa aac tta ctc gat gtc att gac caa gca
376      aga      3358
377      Leu Ala Val Asp Ala Lys Asn Leu Leu Asp Val Ile Asp Gln Ala
W--> 378      Arg
W--> 379                      1030                      1035                      1040
E--> 380      ctg aaa atg ctt ggg cag acg aga cca cac tga gcctccccta
381      ggagcacgtc 3411
382      Leu Lys Met Leu Gly Gln Thr Arg Pro His
W--> 383      1045                      1050
E--> 384      ttgctaccct cttttgaaga tgttctctag ccttccacca gcagcgagga
385      attaacctg 3471
E--> 386      tgtcctcagt cgccagcact tacagctcca acttttttga atgaccatct
387      ggttgaaaaa 3531

```

*same*

RAW SEQUENCE LISTING                      DATE: 02/13/2001  
 PATENT APPLICATION: US/09/757,100              TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw  
 Output Set: N:\CRF3\02132001\I757100.raw

```

E--> 388      tcttttctcat   ataagtttaa   ccacactttg   atttgggttc   attttttgtt
          389      ttgttttttt 3591
E--> 390      caatcatgat   attcagaaaa   atccaggatc   caaaatgtgg   cgtttttcta
          391      agaataaaaa 3651
E--> 392      ttatatgtaa   gcttttaagc   atcatgaaga   acaatttatg   ttcacattaa
          393      gatacgttct 3711
E--> 394      aaagggggat   ggccaagggg   tgacatctta   attcctaaac   taccttagct
          395      gcatagtgga 3771
E--> 396      agaggagagc                               tagaagcaaa
          397
399 <210> SEQ ID NO: 2
400 <211> LENGTH: 1052
401 <212> TYPE: PRT
402 <213> ORGANISM: Homo sapiens
403 <400> SEQUENCE: 2
404      Met Ala Ala Ala Tyr Leu Asp Pro Asn Leu Asn His Thr Pro Asn
E--> 405      Ser
E--> 406      1              5              10              15
407      Ser Thr Lys Thr His Leu Gly Thr Gly Met Glu Arg Ser Pro Gly
E--> 408      Ala
E--> 409      20              25              30
410      Met Glu Arg Val Leu Lys Val Phe His Tyr Phe Glu Ser Asn Ser
E--> 411      Glu
E--> 412      35              40              45
413      Pro Thr Thr Trp Ala Ser Ile Ile Arg His Gly Asp Ala Thr Asp
E--> 414      Val
E--> 415      50              55              60
416      Arg Gly Ile Ile Gln Lys Ile Val Asp Ser His Lys Val Lys His
E--> 417      Val
E--> 418      65              70              75
E--> 419      80
420      Ala Cys Tyr Gly Phe Arg Leu Ser His Leu Arg Ser Glu Glu Val
E--> 421      His
E--> 422      85              90              95
423      Trp Leu His Val Asp Met Gly Val Ser Ser Val Arg Glu Lys Tyr
E--> 424      Glu
E--> 425      100             105             110
426      Leu Ala His Pro Pro Glu Glu Trp Lys Tyr Glu Leu Arg Ile Arg
E--> 427      Tyr
E--> 428      115             120             125
429      Leu Pro Lys Gly Phe Leu Asn Gln Phe Thr Glu Asp Lys Pro Thr
E--> 430      Leu
E--> 431      130             135             140
432      Asn Phe Phe Tyr Gln Gln Val Lys Ser Asp Tyr Met Leu Glu Ile
E--> 433      Ala
E--> 434      145             150             155
E--> 435      160
436      Asp Gln Val Asp Gln Glu Ile Ala Leu Lys Leu Gly Cys Leu Glu
E--> 437      Ile

```

*see item 2  
 on Eva Summary  
 sheet*

## RAW SEQUENCE LISTING

DATE: 02/13/2001

PATENT APPLICATION: US/09/757,100

TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw

Output Set: N:\CRF3\02132001\I757100.raw

```

E--> 438          165          170          175
      439 Arg Arg Ser Tyr Trp Glu Met Arg Gly Asn Ala Leu Glu Lys Lys
E--> 440 Ser
E--> 441          180          185          190
      442 Asn Tyr Glu Val Leu Glu Lys Asp Val Gly Leu Lys Arg Phe Phe
E--> 443 Pro
E--> 444          195          200          205
      445 Lys Ser Leu Leu Asp Ser Val Lys Ala Lys Thr Leu Arg Lys Leu
E--> 446 Ile
E--> 447          210          215          220
      448 Gln Gln Thr Phe Arg Gln Phe Ala Asn Leu Asn Arg Glu Glu Ser
E--> 449 Ile
E--> 450          225          230          235
E--> 451          240
      452 Leu Lys Phe Phe Glu Ile Leu Ser Pro Val Tyr Arg Phe Asp Lys
E--> 453 Glu
E--> 454          245          250          255
      455 Cys Phe Lys Cys Ala Leu Gly Ser Ser Trp Ile Ile Ser Val Glu
E--> 456 Leu
E--> 457          260          265          270
      458 Ala Ile Gly Pro Glu Glu Gly Ile Ser Tyr Leu Thr Asp Lys Gly
E--> 459 Cys
E--> 460          275          280          285
      461 Asn Pro Thr His Leu Ala Asp Phe Thr Gln Val Gln Thr Ile Gln
E--> 462 Tyr
E--> 463          290          295          300
      464 Ser Asn Ser Glu Asp Lys Asp Arg Lys Gly Met Leu Gln Leu Lys
E--> 465 Ile
E--> 466          305          310          315
E--> 467          320
      468 Ala Gly Ala Pro Glu Pro Leu Thr Val Thr Ala Pro Ser Leu Thr
E--> 469 Ile
E--> 470          325          330          335
      471 Ala Glu Asn Met Ala Asp Leu Ile Asp Gly Tyr Cys Arg Leu Val
E--> 472 Asn
E--> 473          340          345          350
      474 Gly Thr Ser Gln Ser Phe Ile Ile Arg Pro Gln Lys Glu Gly Glu
E--> 475 Arg
E--> 476          355          360          365
      477 Ala Leu Pro Ser Ile Pro Lys Leu Ala Asn Ser Glu Lys Gln Gly
E--> 478 Met
E--> 479          370          375          380
      480 Arg Thr His Ala Val Ser Val Ser Glu Thr Asp Asp Tyr Ala Glu
E--> 481 Ile
E--> 482          385          390          395
E--> 483          400
      484 Ile Asp Glu Glu Asp Thr Tyr Thr Met Pro Ser Thr Arg Asp Tyr
E--> 485 Glu
E--> 486          405          410          415

```

*same  
error*

## RAW SEQUENCE LISTING

DATE: 02/13/2001

PATENT APPLICATION: US/09/757,100

TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw

Output Set: N:\CRF3\02132001\I757100.raw

```

487   Ile Gln Arg Glu Arg Ile Glu Leu Gly Arg Cys Ile Gly Glu Gly
E--> 488   Gln
489           420           425           430
490   Phe Gly Asp Val His Gln Gly Ile Tyr Met Ser Pro Glu Asn Pro
E--> 491   Ala
492           435           440           445
493   Leu Ala Val Ala Ile Lys Thr Cys Lys Asn Cys Thr Ser Asp Ser
E--> 494   Val
495           450           455           460
496   Arg Glu Lys Phe Leu Gln Glu Ala Leu Thr Met Arg Gln Phe Asp
E--> 497   His
498           465           470           475
499           480
500   Pro His Ile Val Lys Leu Ile Gly Val Ile Thr Glu Asn Pro Val
E--> 501   Trp
502           485           490           495
503   Ile Ile Met Glu Leu Cys Thr Leu Gly Glu Leu Arg Ser Phe Leu
E--> 504   Gln
505           500           505           510
506   Val Arg Lys Tyr Ser Leu Asp Leu Ala Ser Leu Ile Leu Tyr Ala
E--> 507   Tyr
508           515           520           525
509   Gln Leu Ser Thr Ala Leu Ala Tyr Leu Glu Ser Lys Arg Phe Val
E--> 510   His
511           530           535           540
512   Arg Asp Ile Ala Ala Arg Asn Val Leu Val Ser Ser Asn Asp Cys
E--> 513   Val
514           545           550           555
515           560
516   Lys Leu Gly Asp Phe Gly Leu Ser Arg Tyr Met Glu Asp Ser Thr
E--> 517   Tyr
518           565           570           575
519   Tyr Lys Ala Ser Lys Gly Lys Leu Pro Ile Lys Trp Met Ala Pro
E--> 520   Glu
521           580           585           590
522   Ser Ile Asn Phe Arg Arg Phe Thr Ser Ala Ser Asp Val Trp Met
E--> 523   Phe
524           595           600           605
525   Gly Val Cys Met Trp Glu Ile Leu Met His Gly Val Lys Pro Phe
E--> 526   Gln
527           610           615           620
528   Gly Val Lys Asn Asn Asp Val Ile Gly Arg Ile Glu Asn Gly Glu
E--> 529   Arg
530           625           630           635
531           640
532   Leu Pro Met Pro Pro Asn Cys Pro Pro Thr Leu Tyr Ser Leu Met
E--> 533   Thr
534           645           650           655
535   Lys Cys Trp Ala Tyr Asp Pro Ser Arg Arg Pro Arg Phe Thr Glu

```

*same*

## RAW SEQUENCE LISTING

DATE: 02/13/2001

PATENT APPLICATION: US/09/757,100

TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw

Output Set: N:\CRF3\02132001\I757100.raw

```

E--> 536      Leu
E--> 537      660      665      670
538      Lys Ala Gln Leu Ser Thr Ile Leu Glu Glu Glu Lys Ala Gln Gln
E--> 539      Glu
E--> 540      675      680      685
541      Glu Arg Met Arg Met Glu Ser Arg Arg Gln Ala Thr Val Ser Trp
E--> 542      Asp
E--> 543      690      695      700
544      Ser Gly Gly Ser Asp Glu Ala Pro Pro Lys Pro Ser Arg Pro Gly
E--> 545      Tyr
E--> 546      705      710      715
E--> 547      720
548      Pro Ser Pro Arg Ser Ser Glu Gly Phe Tyr Pro Ser Pro Gln His
E--> 549      Met
E--> 550      725      730      735
551      Val Gln Thr Asn His Tyr Gln Val Ser Gly Tyr Pro Gly Ser His
E--> 552      Gly
E--> 553      740      745      750
554      Ile Thr Ala Met Ala Gly Ser Ile Tyr Pro Gly Gln Ala Ser Leu
E--> 555      Leu
E--> 556      755      760      765
557      Asp Gln Thr Asp Ser Trp Asn His Arg Pro Gln Glu Ile Ala Met
E--> 558      Trp
E--> 559      770      775      780
560      Gln Pro Asn Val Glu Asp Ser Thr Val Leu Asp Leu Arg Gly Ile
E--> 561      Gly
E--> 562      785      790      795
E--> 563      800
564      Gln Val Leu Pro Thr His Leu Met Glu Glu Arg Leu Ile Arg Gln
E--> 565      Gln
E--> 566      805      810      815
567      Gln Glu Met Glu Glu Asp Gln Arg Trp Leu Glu Lys Glu Glu Arg
E--> 568      Phe
E--> 569      820      825      830
570      Leu Lys Pro Asp Val Arg Leu Ser Arg Gly Ser Ile Asp Arg Glu
E--> 571      Asp
E--> 572      835      840      845
573      Gly Ser Leu Gln Gly Pro Ile Gly Asn Gln His Ile Tyr Gln Pro
E--> 574      Val
E--> 575      850      855      860
576      Gly Lys Pro Asp Pro Ala Ala Pro Pro Lys Lys Pro Pro Arg Pro
E--> 577      Gly
E--> 578      865      870      875
E--> 579      880
580      Ala Pro Gly His Leu Gly Ser Leu Ala Ser Leu Ser Ser Pro Ala
E--> 581      Asp
E--> 582      885      890      895
583      Ser Tyr Asn Glu Gly Val Lys Leu Gln Pro Gln Glu Ile Ser Pro
E--> 584      Pro

```

RAW SEQUENCE LISTING                      DATE: 02/13/2001  
 PATENT APPLICATION: US/09/757,100              TIME: 08:09:56

Input Set : N:\Crif3\02052001\I757100.raw  
 Output Set: N:\CRF3\02132001\I757100.raw

```

E--> 585           900           905           910
586   Pro Thr Ala Asn Leu Asp Arg Ser Asn Asp Lys Val Tyr Glu Asn
E--> 587   Val
E--> 588           915           920           925
589   Thr Gly Leu Val Lys Ala Val Ile Glu Met Ser Ser Lys Ile Gln
E--> 590   Pro
E--> 591           930           935           940
592   Ala Pro Pro Glu Glu Tyr Val Pro Met Val Lys Glu Val Gly Leu
E--> 593   Ala
E--> 594           945           950           955
E--> 595   960
596   Leu Arg Thr Leu Leu Ala Thr Val Asp Glu Thr Ile Pro Leu Leu
E--> 597   Pro
E--> 598           965           970           975
599   Ala Ser Thr His Arg Glu Ile Glu Met Ala Gln Lys Leu Leu Asn
E--> 600   Ser
E--> 601           980           985           990
602   Asp Leu Gly Glu Leu Ile Asn Lys Met Lys Leu Ala Gln Gln Tyr
E--> 603   Val
E--> 604           995           1000           1005
605   Met Thr Ser Leu Gln Gln Glu Tyr Lys Lys Gln Met Leu Thr Ala
E--> 606   Ala
E--> 607           1010           1015           1020
608   His Ala Leu Ala Val Asp Ala Lys Asn Leu Leu Asp Val Ile Asp
E--> 609   Gln
E--> 610           025           1030           1035
E--> 611           1040
612   Ala Arg Leu Lys Met Leu Gly Gln Thr Arg Pro His
E--> 613           1045           1050
615 <210> SEQ ID NO: 3
616 <211> LENGTH: 20
617 <212> TYPE: DNA
618 <213> ORGANISM: Artificial Sequence
619 <220> FEATURE:
620 <223> OTHER INFORMATION: antisense sequence
621 <400> SEQUENCE: 3
E--> 622   ccgcgggctc           acagtggctcg
623           20
625 <210> SEQ ID NO: 4
626 <211> LENGTH: 20
627 <212> TYPE: DNA
628 <213> ORGANISM: Artificial Sequence
629 <220> FEATURE:
630 <223> OTHER INFORMATION: antisense sequence
631 <400> SEQUENCE: 4
E--> 632   ggcgcggtga           agcgaaggca
633           20
635 <210> SEQ ID NO: 5
636 <211> LENGTH: 20

```

*same*

*see item 1  
on Enr  
summary sheet*



RAW SEQUENCE LISTING                      DATE: 02/13/2001  
PATENT APPLICATION: US/09/757,100              TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw  
Output Set: N:\CRF3\02132001\I757100.raw

```
637 <212> TYPE: DNA
638 <213> ORGANISM: Artificial Sequence
639 <220> FEATURE:
640 <223> OTHER INFORMATION: antisense sequence
641 <400> SEQUENCE: 5
E--> 642      cagttctgct      cggaccgcgg
643      20
645 <210> SEQ ID NO: 6
646 <211> LENGTH: 20
647 <212> TYPE: DNA
648 <213> ORGANISM: Artificial Sequence
649 <220> FEATURE:
650 <223> OTHER INFORMATION: antisense sequence
651 <400> SEQUENCE: 6
E--> 652      gaaactgcag      aaggcactga
653      20
655 <210> SEQ ID NO: 7
656 <211> LENGTH: 20
657 <212> TYPE: DNA
658 <213> ORGANISM: Artificial Sequence
659 <220> FEATURE:
660 <223> OTHER INFORMATION: antisense sequence
661 <400> SEQUENCE: 7
E--> 662      ttctcccttc      cgttattctt
663      20
665 <210> SEQ ID NO: 8
666 <211> LENGTH: 20
667 <212> TYPE: DNA
668 <213> ORGANISM: Artificial Sequence
669 <220> FEATURE:
670 <223> OTHER INFORMATION: antisense sequence
671 <400> SEQUENCE: 8
E--> 672      ctagatgcta      ggtatctgtc
673      20
675 <210> SEQ ID NO: 9
676 <211> LENGTH: 20
677 <212> TYPE: DNA
678 <213> ORGANISM: Artificial Sequence
679 <220> FEATURE:
680 <223> OTHER INFORMATION: antisense sequence
681 <400> SEQUENCE: 9
E--> 682      ttttgctaga      tgctaggtat
683      20
685 <210> SEQ ID NO: 10
686 <211> LENGTH: 20
687 <212> TYPE: DNA
688 <213> ORGANISM: Artificial Sequence
689 <220> FEATURE:
690 <223> OTHER INFORMATION: antisense sequence
```

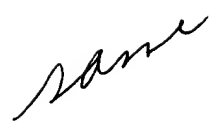
*same*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/757,100

DATE: 02/13/2001  
TIME: 08:09:56

Input Set : N:\Crf3\02052001\I757100.raw  
Output Set: N:\CRF3\02132001\I757100.raw

691 <400> SEQUENCE: 10  
E--> 692 ggtaagcagc tgccattatt  
693 20  
695 <210> SEQ ID NO: 11  
696 <211> LENGTH: 20  
697 <212> TYPE: DNA  
698 <213> ORGANISM: Artificial Sequence  
699 <220> FEATURE:  
700 <223> OTHER INFORMATION: antisense sequence  
701 <400> SEQUENCE: 11  
E--> 702 agtaccagg tgagtcttag  
703 20  
705 <210> SEQ ID NO: 12  
706 <211> LENGTH: 20  
707 <212> TYPE: DNA  
708 <213> ORGANISM: Artificial Sequence  
709 <220> FEATURE:  
710 <223> OTHER INFORMATION: antisense sequence  
711 <400> SEQUENCE: 12  
E--> 712 cctgacatca gtagcatctc  
713 20  
715 <210> SEQ ID NO: 13  
716 <211> LENGTH: 20  
717 <212> TYPE: DNA  
718 <213> ORGANISM: Artificial Sequence  
719 <220> FEATURE:  
720 <223> OTHER INFORMATION: antisense sequence  
721 <400> SEQUENCE: 13  
E--> 722 gttggcttat cttcagtaaa  
723 20  
725 <210> SEQ ID NO: 14  
726 <211> LENGTH: 20  
727 <212> TYPE: DNA  
728 <213> ORGANISM: Artificial Sequence  
729 <220> FEATURE:  
730 <223> OTHER INFORMATION: antisense sequence  
731 <400> SEQUENCE: 14  
E--> 732 ggtagggat ggtgccgtca  
733 20  
735 <210> SEQ ID NO: 15  
736 <211> LENGTH: 20  
737 <212> TYPE: DNA  
738 <213> ORGANISM: Artificial Sequence  
739 <220> FEATURE:  
740 <223> OTHER INFORMATION: antisense sequence  
741 <400> SEQUENCE: 15  
E--> 742 tgttggtttc caatcggacc  
743 20  
745 <210> SEQ ID NO: 16



RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/757,100

DATE: 02/13/2001  
TIME: 08:09:56

Input Set : N:\Cr3\02052001\I757100.raw  
Output Set: N:\CRF3\02132001\I757100.raw

746 <211> LENGTH: 20  
747 <212> TYPE: DNA  
748 <213> ORGANISM: Artificial Sequence  
749 <220> FEATURE:  
750 <223> OTHER INFORMATION: antisense sequence  
751 <400> SEQUENCE: 16  
E--> 752 ctaggggagg ctcagtgtgg  
753 20  
755 <210> SEQ ID NO: 17  
756 <211> LENGTH: 20  
757 <212> TYPE: DNA  
758 <213> ORGANISM: Artificial Sequence  
759 <220> FEATURE:  
760 <223> OTHER INFORMATION: antisense sequence  
761 <400> SEQUENCE: 17  
E--> 762 attcctcgct gctggtggaa  
763 20  
765 <210> SEQ ID NO: 18  
766 <211> LENGTH: 20  
767 <212> TYPE: DNA  
768 <213> ORGANISM: Artificial Sequence  
769 <220> FEATURE:  
770 <223> OTHER INFORMATION: antisense sequence  
771 <400> SEQUENCE: 18  
E--> 772 tttcaaccag atggtcattc  
773 20  
775 <210> SEQ ID NO: 19  
776 <211> LENGTH: 20  
777 <212> TYPE: DNA  
778 <213> ORGANISM: Artificial Sequence  
779 <220> FEATURE:  
780 <223> OTHER INFORMATION: antisense sequence  
781 <400> SEQUENCE: 19  
E--> 782 ttctgaatat catgattgaa  
783 20  
785 <210> SEQ ID NO: 20  
786 <211> LENGTH: 20  
787 <212> TYPE: DNA  
788 <213> ORGANISM: Artificial Sequence  
789 <220> FEATURE:  
790 <223> OTHER INFORMATION: antisense sequence  
791 <400> SEQUENCE: 20  
E--> 792 catgatgctt aaaagcttac  
793 20  
795 <210> SEQ ID NO: 21  
796 <211> LENGTH: 20  
797 <212> TYPE: DNA  
798 <213> ORGANISM: Artificial Sequence  
799 <220> FEATURE:

*same*

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/757,100

DATE: 02/13/2001  
TIME: 08:09:56

Input Set : N:\Crif3\02052001\I757100.raw  
Output Set: N:\CRF3\02132001\I757100.raw

800 <223> OTHER INFORMATION: antisense sequence  
801 <400> SEQUENCE: 21  
E--> 802       aatgtgaaca  
803       20

taaattgttc

*name*

*FYI:* Please review the  
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to  
<223> fields of each sequence which presents at least one n or Xaa.

## VERIFICATION SUMMARY

DATE: 02/13/2001

PATENT APPLICATION: US/09/757,100

TIME: 08:09:57

Input Set : N:\Crf3\02052001\I757100.raw

Output Set: N:\CRF3\02132001\I757100.raw

L:32 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:50 SEQ:1

M:254 Repeated in SeqNo=1

L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:46 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:55 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:61 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:62 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:66 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:67 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:71 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:76 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:77 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:81 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:82 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:87 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:88 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:92 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:93 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:97 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:98 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:102 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:103 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:108 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:113 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:118 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:134 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:139 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:140 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:144 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:145 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:149 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:154 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:159 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:160 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1

VERIFICATION SUMMARY                      DATE: 02/13/2001  
PATENT APPLICATION: US/09/757,100        TIME: 08:09:57

Input Set : N:\Crf3\02052001\I757100.raw  
Output Set: N:\CRF3\02132001\I757100.raw

L:165 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:166 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:171 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:405 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2  
M:332 Repeated in SeqNo=2  
L:622 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:3  
L:632 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:4  
L:642 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:5  
L:652 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:6  
L:662 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:7  
L:672 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:8  
L:682 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:9  
L:692 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:10  
L:702 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:11  
L:712 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:12  
L:722 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:13  
L:732 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:14  
L:742 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:15  
L:752 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:16  
L:762 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:17  
L:772 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:18  
L:782 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:19  
L:792 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:20  
L:802 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:21  
L:812 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:22  
L:822 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:23  
L:832 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:24  
L:842 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:25  
L:852 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:26  
L:862 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:27  
L:872 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:28  
L:882 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:29  
L:892 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:30  
L:902 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:31  
L:912 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:32  
L:922 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:33  
L:932 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:34  
L:942 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:35  
L:952 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:36  
L:962 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:37  
L:972 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:38  
L:982 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:39  
L:992 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:40  
L:1002 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:41  
L:1012 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:15 SEQ:42  
L:1022 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:43  
L:1034 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:44  
L:1034 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:44